

Resource Summary Report

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CheckM2

RRID:SCR_026897

Type: Tool

Proper Citation

CheckM2 (RRID:SCR_026897)

Resource Information

URL: <https://github.com/chklovski/CheckM2>

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Description: Software tool to predict completeness and contamination of genomic bins. Used for predicting genome quality of metagenome-assembled genomes. Assessing microbial genome quality using machine learning.

Resource Type: source code, software application, software resource

Defining Citation: [PMID:37500759](#), [PMID:38514780](#)

Keywords: predicting genome quality, metagenome-assembled genomes, genomic bins, microbial genome quality,

Availability: Free, Available for download, Freely available,

Resource Name: CheckM2

Resource ID: SCR_026897

License: GNU GPN v3

Record Creation Time: 20250503T055712+0000

Record Last Update: 20260815T183241+0000

Ratings and Alerts

No rating or validation information has been found for CheckM2.

No alerts have been found for CheckM2.

Data and Source Information

Usage and Citation Metrics

We found 72 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Fernández-Trapote E, et al. (2026) Microbiome and resistome successions in pig carcasses and fresh pork meat throughout slaughtering, processing and shelf-life. *Microbiome*, 14(1), 67.

Mitra M, et al. (2026) Complete genomic sequences of the single chromosome and four putative plasmids of *Sphingobium yanoikuyae* strain CC4533. *Microbiology resource announcements*, 15(2), e0118125.

Davina-Nunez C, et al. (2026) Pangenomic analysis reveals metabolic adaptation of *Haemophilus parainfluenzae* to the urogenital tract. *Virulence*, 17(1), 2613506.

Washeleski E, et al. (2026) The WormFood CURE: Screening for bioactive metabolites that antagonize the *Caenorhabditis elegans* Ras signaling pathway. *bioRxiv : the preprint server for biology*.

Zhang XX, et al. (2026) Gut microbiota response to *Enterocytozoon bieneusi* infection in wild rodents: enhanced vitamin B and K2 biosynthesis pathways. *BMC genomics*, 27(1).

Moreira G, et al. (2026) Antimicrobial Resistance, Virulence Factors and Plasmid Replicon Patterns of *Klebsiella pneumoniae* and *Klebsiella grimontii* Isolates from Bovine Mastitic Milk in the Northwest of Portugal: Pilot Genomic Characterization. *Antibiotics (Basel, Switzerland)*, 15(2).

Shoaib M, et al. (2026) First co-emergence of plasmid-borne tigecycline resistance genes *tet(X4)* and *tmexCD1-toprJ1* in *Raoultella ornithinolytica* isolated from retail pork: insights from global genomic analysis. *Current research in food science*, 12, 101362.

Baek JH, et al. (2026) Genome-resolved insights into the ecology, metabolic potential, salt-stress adaptation, and safety of *Staphylococcus* in traditional Korean soybean fermentation. *NPJ science of food*, 10(1).

Kück AC, et al. (2026) Host species-specific gene expression by a widespread and flexible chemosynthetic symbiont. *The ISME journal*, 20(1).

Wan Y, et al. (2026) Genomic and molecular characterisation of a KPC-producing *Klebsiella pneumoniae* clinical isolate resistant to meropenem-vaborbactam, imipenem-relebactam, and ceftazidime-avibactam. *BMC genomic data*, 27(1).

Hamm JN, et al. (2026) New lineages provide insights into the convergent evolution of extreme salt adaptation within symbiotic Archaea. *Molecular biology and evolution*, 43(5).

Fang C, et al. (2026) Fourteen-year genomic surveillance of pediatric invasive *Streptococcus pneumoniae*: genomic and pan-genomic characterization. *BMC*

microbiology, 26(1).

Bowerman KL, et al. (2026) A molecular inventory of the faecal microbiomes of 23 marsupial species. *Microbial genomics*, 12(1).

Zhou H, et al. (2026) One Health genomics reveals niche-specific lineage replacement in *Salmonella* Enteritidis. *National science review*, 13(11), nwag275.

Mbwana JR, et al. (2026) Molecular characterisation of extended-Spectrum-Beta-lactamase-producing *Klebsiella pneumoniae* among children and chicken in the rural Korogwe District, Tanzania. *One health (Amsterdam, Netherlands)*, 23, 101472.

Guo J, et al. (2026) Mobile genetic elements shape microbial diversity and functions in thawing permafrost soils. *Nature microbiology*, 11(7), 1800.

Takei S, et al. (2026) Isolation and identification of *Pseudoxanthomonas winnipegensis* from blood culture by MALDI-MS. *Frontiers in cellular and infection microbiology*, 16, 1755501.

Valença CAS, et al. (2026) Genome-guided antimicrobial potential of *Bacillus stercoris* from coastal sand with activity against multidrug-resistant bacteria, including MRSA. *International microbiology : the official journal of the Spanish Society for Microbiology*, 29(5), 713.

Wunderer M, et al. (2026) Comparative phenotypic and genomic analysis of the methanogen *Methanomethylovorans thermophila* L2FAW and its phylogenomic placement within the Genome Taxonomy Database. *Access microbiology*, 8(5).

Steegmüller T, et al. (2026) Third Generation Genome Sequencing of the Endobacterium *Corynebacterium kroppenstedtii* subsp. *demodicis* Reveals Details of Its Microbe-Host-Interaction With the Most Complex Human Commensal, *Demodex folliculorum*. *Environmental microbiology reports*, 18(3), e70374.